

MDEADRALLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRRDQA  
RQLIIDLETRGSQAL  
PLFISCLEDTGQDMLASFLRTNRQAGKLSKPTLENLTPVVLRPEIRKPEVLRPETPR  
PVDIGSGGFGDVG  
ALESLRGNADLAYILSMEPCGHCLIINNVNFRESGLRTRTGSNIDCEKLRRRFSSL  
HFMVEVKGDLTAK  
KMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGCPVSVEKIVNI  
FNGTSCPSLGGKPK  
LFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAISSLP  
TPSDIFVSYSTFPG  
FVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIVKQMPGCFN  
FLRKKLFFKTS

**FIG. I**

1 GCCATGGACG AAGCGGATCG GCGGCTCCTG CGGC GGCTGCGGCT  
51 GGTGGAAGAG CTGCAGGTGG ACCAGCTCTG GGACGTCCTG CTGAGCCGCG  
101 AGCTGTTCA GCCCCATATG ATCGAGGACA TCCAGCGGGC AGGCTCTGGA  
151 TCTCGGCCGG ATCAGGCCAG GCAGCTGATC ATAGATCTGG AGACTCGAGG  
201 GAGTCAGGCT CTTCTTGT TCATCTCCTG CTTAGAGGAC ACAGGCCAGG  
251 ACATGCTGGC TTCGTTCTG CGAACTAAC A GGCAAGCAGG AAAGTTGTCG  
301 AAGCCAACCC TAGAAAACCT TACCCCAGTG GTGCTCAGAC CAGAGATTG  
351 CAAACCAGAG GTTCTCAGAC CGGAAACACC CAGACCAGTG GACATTGGTT  
401 CTGGAGGATT CGGTGATGTC GGTGCTCTG AGAGTTGAG GGGAAATGCA  
451 GATTGGCTT ACATCCTGAG CATGGAGCCC TGTGGCCACT GCCTCATTAT  
501 CAACAATGTG AACCTCTGCC GTGAGTCCGG GCTCCGCACC CGCACTGGCT  
551 CCAACATCGA CTGTGAGAAG TTGCGCGTC GCTTCTCCTC GCTGCATTTC  
601 ATGGTGGAGG TGAAGGGCGA CCTGACTGCC AAGAAAATGG TGCTGGCTTT  
651 GCTGGAGCTG GCGCGGCAGG ACCACGGTGC TCTGGACTGC TGCGTGGTGG  
701 TCATTCTCTC TCACGGCTGT CAGGCCAGCC ACCTGCAGTT CCCAGGGCT

**FIG. 2A**

751 GTCTACGGCA CAGATGGATG CCCTGTGTCG GTCGAGAAGA TTGTGAACAT

801 CTTCAATGGG ACCAGCTGCC CCAGCCTGGG AGGGAAGCCC AAGCTCTTT

851 TCATCCAGGC CTGTGGTGGG GAGCAGAAAG ACCATGGGTT TGAGGTGGCC

901 TCCACTTCCC CTGAAGACGA GTCCCCTGGC AGTAACCCCG AGCCAGATGC

951 CACCCCGTTC CAGGAAGGTT TGAGGACCTT CGACCAGCTG GACGCCATAT

1001 CTAGTTGCC CACACCCAGT GACATCTTG TGTCTACTC TACTTCCCA

1051 GGTTTGTTC CCTGGAGGGA CCCAAGAGT GGCTCTGGT ACGTTGAGAC

1101 CCTGGACGAC ATCTTGAGC AGTGGGCTCA CTCTGAAGAC CTGCAGTCCC

1151 TCCTGCTTAG GGTGCTAAT GCTGTTCGG TGAAAGGGAT TTATAAACAG

1201 ATGCCTGGTT GCTTAATT CCTCCGGAAA AAACCTTCT TTAAAACATC

1251 ATAAGGCCAG GGCCCCCAC CCTGCCTTAT CTTGCACCCCA AAAGCTTCC

1301 TGCCCCAGGC CTGAAAGAGG CTGAGGCCTG GACTTCTG CAACTCAAGG

1351 ACTTTGNAGC CGGCACACAGGG TCTGCTCTT CTCTGCCAGT GACAGACAGG

1401 CTCTTAGCAG CTTCCAGATT GACGACAAGT GCTGAACAGT GGAGGAAGAG

1451 GGACAGATGA ATGCCGTGGA TTGCACGTGG NCTCTTGAGC AGTGGCTGGT

FIG. 2B

1501 CCAGGGCTAG TGACTTGGTG TCCCATGATC CCTGTGTTGG TCTCTAGGAG

1551 CAGGGATTAA CCTCTGCAC ACTGACAT

## FIG. 2C

CTGACTGCCAAGAAAATGGTGGCTGGCTTGCTGGAGCTGG 40  
CGCGGCAGGACCACGGTGTCTGGACTGCTGCGTGGTGGT 80  
CATTCTCTCTCACGGCTGTCAAGGCCAGCCACCTGCAGTTC 120  
CCAGGGCTGTCTACGGCACAGATGGATGCCCTGTGTCGG 160  
TCGAAAAGATTGTGAACATCTTCAATGGGACCAGCTGCC 200  
CAGCCTGGGAGGGAAGCCCAAGCTCTTTCATCCAGGCC 240  
TGTGGTGGGGAGCAGAAAGACCATGGGTTGAGGTGGCCT 280  
CCACTTCCCCTGAAGACGAGTCCCCTGGCAGTAACCCCGA 320  
GCCAGATGCCACCCCGTCCAGGAAGGTTGAGGACCTTC 360  
GACCAGCTGGACGCCATATCTAGTTGCCACACCCAGTG 400  
ACATCTTGTGTCTACTCTACTTCCCAGGTTTGTTC 440  
CTGGAGGGACCCAAGAGTGGCTCTGGTACGTTGAGACC 480  
CTGGACGACATCTTGAAGCAGTGGCTCACTCTGAAGACC 520  
TGCAGTCCCTCTGCTTAGGGTCGCTAATGCTGTTGGT 560  
GAAAGGGATTATAAACAGATGCCTGGTTGCTTTAATTTC 600  
CTCCGGAAAAAACTTTCTTTAAAACATCATAAGGCAG 639

## FIG. 3

MVLALLELARQDHGALDCCV 20  
VVILSHGCQASHLQFPGAVY 40  
GTDGCPVSVEKIVNIFNGTS 60  
CPSLGGKPKLFFIQACGGEQ 80  
KDHGFEVASTSPEDESPGSN 100  
PEPDATPFQEGLRTFDQLDA 120  
ISSLPTPSDIFVSYSTFPGF 140  
VSWRDPKSGSWYVETLDDIF 160  
EQWAHSEDLQSLLLRVANAV 180  
SVKGIIYKQMPGCFNFLRKKL 200  
FFM 203

**FIG. 4**

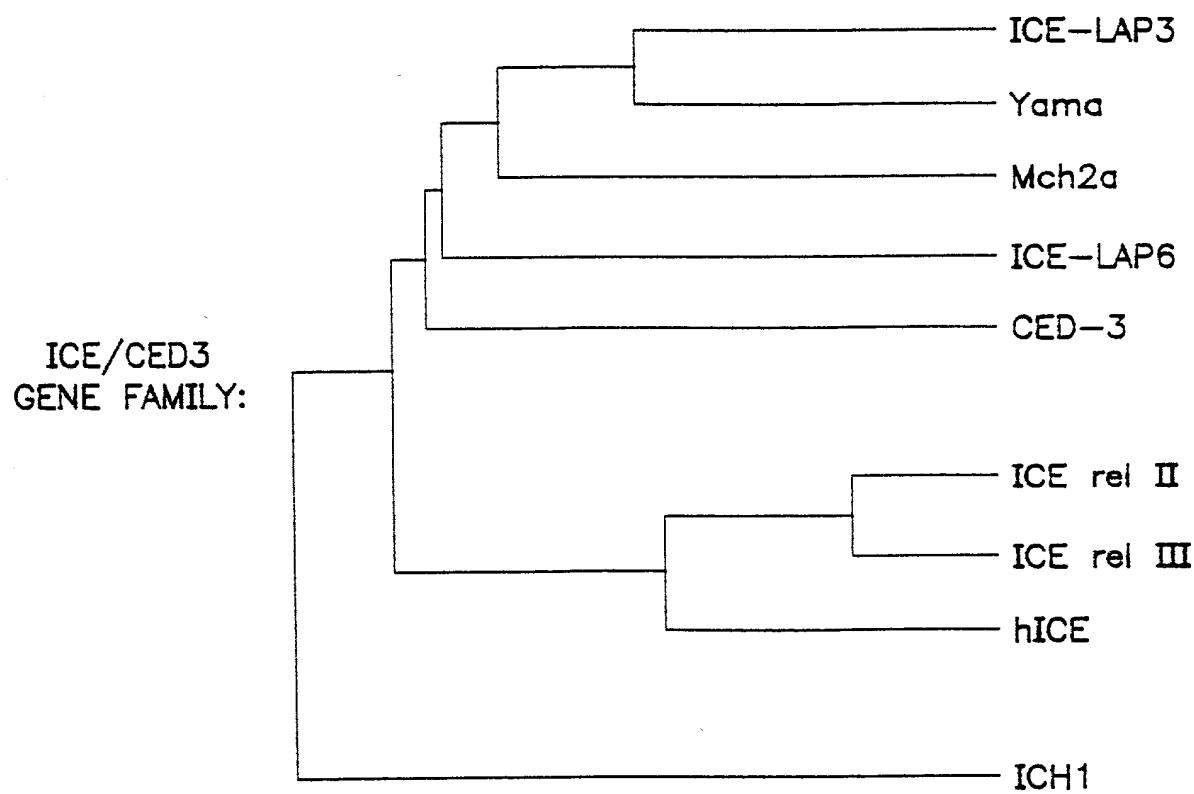


FIG. 5

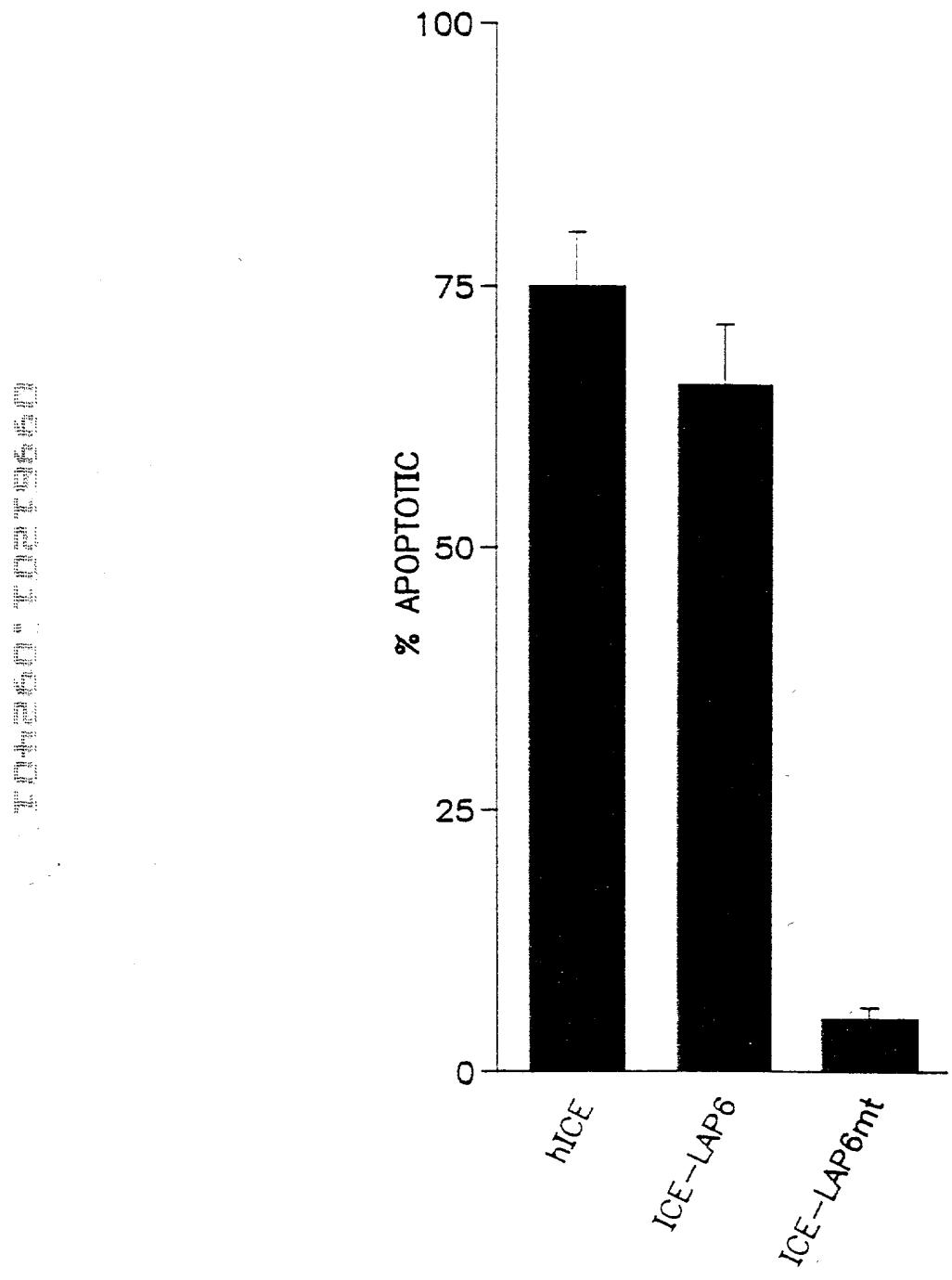


FIG. 6